

ESP 121: Lab 4

Two-species models: parasitism and competition

1. Open `NicholsonBailey.R`. This runs the Nicholson Bailey model, without host density dependence in the top plot, and with host density dependence in the bottom plot.

(a) For the basic model, without host density dependence (top plot):

$$\begin{aligned}H_{t+1} &= \lambda H_t e^{-aP_t} \\P_{t+1} &= cH_t(1 - e^{-aP_t})\end{aligned}$$

the script runs the model given a starting point determined by the value you enter for `diff`, which gets multiplied by the values for the host and parasitoid abundances at the internal equilibrium (given $\lambda = e^{0.5}$, $a = 0.001$, and $c = 3$). If `diff`=1 it starts exactly at the equilibrium, if `diff`=1.01 they both start with values 1% greater than their equilibrium values, etc. The script plots the output of both host and parasitoid over time. Choose a value for `diff` representative of starting in the neighborhood of the internal equilibrium, and describe the dynamics (host and parasitoid abundance over time) that result.

(b) For the model with Ricker-style density dependence for the host (bottom plot):

$$\begin{aligned}H_{t+1} &= H_t e^{r(1-H_t/K)-aP_t} \\P_{t+1} &= cH_t(1 - e^{-aP_t})\end{aligned}$$

the script runs the model for different values of K that you enter (given $r = 0.5$, $a = 0.001$, and $c = 3$) and plots the resulting host and parasitoid trajectories. Describe how the dynamics change with increasing K . Why does this occur?

2. Download `compFit.R`, `parameciumrK.txt`, and `paramecium2.txt` all to the same folder (all to the desktop works). Then, in R, change your directory to that folder/location (Session menu, Set Working Directory). `parameciumrK.txt` and `paramecium2.txt` contain data from Gause's (1935) experiments on two species of *Paramecium* (single-celled organisms; check out <https://microbewiki.kenyon.edu/index.php/Paramecium> for more about them), with the former containing the r and K values from a fit of a logistic model to each grown separately, and the latter containing the time series of both species in competition. The R script fits a Lotka-Volterra competition model:

$$\begin{aligned}\frac{dn_1}{dt} &= \frac{r_1 n_1}{K_1} (K_1 - n_1 - \alpha_{12} n_2) \\ \frac{dn_2}{dt} &= \frac{r_2 n_2}{K_2} (K_2 - n_2 - \alpha_{21} n_1)\end{aligned}$$

to the time series of the species in competition, given the r and K values from the data of each species grown separately, to find the values for α_{ij} . It then plots both the real and simulated data for each species as well as reports all parameter values at the prompt. Run the script. If Gause had run the experiment for longer, what do you expect the eventual outcome would be? Why? (Hint: you can use the calculator function of R and information from your class notes to answer this problem.)